Amendments to the Specification

This amendment to the specification will replace all prior versions, for the sections indicated:

Please amend the paragraph on page 30, line 19 – page 31, line 5, as follows:

Appropriate probes may be designed to hybridize to specific regions of the CETP gene. Primers useful for amplifying regions of the CETP gene will be apparent to one of skill in the art in light of the present disclosure. Reasonable primers include those which hybridize within about 1 kb of the designated primer, and which further are anywhere from about 17 bp to about 27 bp in length. A general guideline for designing primers for amplification of unique human chromosomal genomic sequences is that they possess a melting temperature of at least about 50°C, wherein an approximate melting temperature can be estimated using the formula T_{melt} = [2 x (# of A or T) + 4 x (# of G or C)]. These probes may incorporate other regions of the relevant genomic locus, including intergenic sequences. Indeed, the CETP gene spans some 25,000 base pairs and, assuming an average of one single nucleotide polymorphism every 1,000 base pairs, includes some 25 SNP loci alone. Yet other polymorphisms available for use with the immediate invention are obtainable from various public sources. For example, the human genome database collects intragenic SNPs, is searchable by sequence and currently contains approximately 2,700 entries ~~(http://hgbase.interactiva.de)~~. Also available is a human polymorphism database maintained by the Massachusetts Institute of Technology (MIT SNP database ~~http://www.genome.wi.mit.edu/SNP/human/index.html)~~). From such sources, SNPs as well as other human polymorphisms may be found.